

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw model

Run on: April 12, 2004, 10:18:37 ; Search time 21 seconds  
(without alignments)  
1543.645 Million cell updates/sec

Title: US-10-025-730-1

Perfect score: 1704

Sequence: 1 MKKPLFSKSHKNPAEIVKI.....FADENYLIKQIRIDIKTAP 337

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

1: PIR.78:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1376	80.8	341 2 157997	hypothetical calci
2	1063.5	62.4	377 2 116651	hypothetical prote
3	1006.5	59.1	338 2 127129	hypothetical prote
4	834.5	49.0	329 2 150117	mod5 homolog (imp
5	685	40.2	305 2 671441	hypothetical prote
6	632	37.1	348 2 884488	hypothetical prote
7	485	28.5	399 2 534681	hypothetical prote
8	143.5	7.9	339 2 133477	hypothetical prote
9	134.5	7.4	677 2 164574	DNA topoisomerase
10	128	7.5	430 2 164709	hypothetical prote
11	125.5	7.4	298 2 871685	hypothetical prote
12	125.5	7.4	1642 2 108880	NMDA receptor-bind
13	123.5	7.2	1285 2 872420	hypothetical prote
14	120	7.0	1175 2 1175	hypothetical prote
15	118.5	7.0	959 2 100246	DNA polymerase V -
16	115	6.7	474 2 571322	glutathione syntha
17	113.5	6.7	833 2 143446	hypothetical prote
18	112.5	6.6	1411 2 555133	hypothetical prote
19	111.5	6.5	725 1 105016	hyaluronan recepto
20	111.5	6.5	2401 2 128476	rhodopy protein -
21	111	6.5	2166 2 670163	hypothetical prote
22	111	6.5	2819 2 890551	conserved hypotnet
23	109.5	6.4	457 2 882911	hypothetical prote
24	109.5	6.4	978 2 470387	conserved hypotnet
25	109.5	6.4	1830 2 882909	conserved hypotnet
26	109	6.4	695 2 107283	hypothetical prote
27	109	6.4	1401 2 511577	alpha-lactotoxin p
28	108.5	6.4	442 2 118507	hypothetical prote
29	108.5	6.4	952 2 150451	hypothetical coile

30	108.5	6.4	1163	2	D64315	type I restriction
31	108	6.3	568	2	S73254	replication helica
32	107.5	6.3	483	3	140055	positive trans-act
33	107.5	6.3	855	2	E90106	importin beta-1 su
34	107.5	6.3	1042	2	G64514	type I restriction
35	107.5	6.3	1726	1	SAZQGM	major mercozole su
36	107.5	6.3	1726	2	A45948	phosphoprotein pho
37	107	6.3	570	2	S68686	sp8 protein - figs
38	107	6.3	1173	2	T43527	myosin-like coiled
39	107	6.3	1727	2	T50073	glutathione syntha
40	106	6.2	474	2	S56748	hypothetical prote
41	106	6.2	1295	2	T24587	protein kinase hom
42	105.5	6.2	781	2	T00456	GTPase-activating
43	105.5	6.2	847	2	A56039	hypothetical prote
44	105.5	6.2	1091	2	T34107	hypothetical prote
45	105.5	6.2	1619	2	T18499	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

157997  
hypothetical calcium-binding protein - mouse

C/Species: Mus sp. (mouse)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #ext\_change 19-May-2000

C/Accession: 157997

R/Miyamoto, H.; Matsushiro, A.; Nozaki, M.

Mol. Reprod. Dev. 34, 1-7, 1993

A/Title: Molecular cloning of a novel mRNA sequence expressed in cleavage stage mou

A/Reference number: 157997; MUID:3119656; PMID:8418609

A/Accession: 157997

A/Status: preliminary; translated from GB/EHBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-341 <RES>

A/Cross-References: GB:S51858; NID:9262933; PIDN:AA24801.1; PID:9262934

C/Superfamily: Saccharomyces hypothetical protein YKU189w

C/Keywords: calcium binding

Query Match 80.8%; Score 1376; DB 2; Length 341;

Best Local Similarity 80.7%; Pred. No. 7.9e-85; Matches 272; Conservative 32; Mismatches 29; Indels 4; Gaps 2;

QY	4	MPF-PSKSHKNPAEIVKILKDNALIEKQ---	DKTDXSEVSKSLQMKSLGCTNEK	59
DB	1	MPFPGKSHKSPADIVKILKESMAVLEKODISDKAKAKTEEVSKVLVAKKILVGTNEK		60
QY	60	EPPTAAVAKQIAOEIYSSGLVTLADQLDFEGKDYQVQIFNNILRQIGTRSPVETI		119
DB	61	EPQTAVAQIAOEIYNSGLVTLADQLDFEGKDYQVQIFNNILRQIGTRSPVETI		120
QY	120	SAHPHILFMLKGYAEVQIALRCGIMLRBECIRHEPIAKIILFENQFRDFKVELSTEDI		179
DB	121	CQOQIILFMLKGYSEPEIALNCGIMLRBECIRHEPIAKIILFENQFRDFKVELSTEDI		180
QY	180	ASDAATATKDLITRHKIVADFLFQNDTIFEDYEKLQSENVYTRQSLKLGELIIDR		239
DB	181	ASDAATATKDLITRHKIVADFLFQNDTIFEDYEKLQSENVYTRQSLKLGELIIDR		240
QY	240	HNFAIMTKYISKPENLKLMMNLADKSPNIOFEAFVFKVFAVSPKPTOPIVEILKNOP		299
DB	241	HNFTIMTKYISKPENLKLMMNLADKSPNIOFEAFVFKVFAVSPKPTOPIVEILKNOP		300
QY	300	KLIEPLSFQKERTDDQFADENYLIKQIRIDIKTAP		336
DB	301	KLIEPLSKFQNDRTEDQFADENYLIKQIRIDIKTAP		337

##### RESULT 2

11651  
hypothetical protein R02E12.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #ext\_change 18-Feb-2000